

16	2024.5	30.8	2259	2	Q86MA9_ANOGA	Q86ma9 anopheles g
17	2024	30.8	479	2	Q4SZJ7_TETNG	Q4szj7 tetraodon n
18	1965	29.9	401	2	Q4G034_RAT	Q4g034 rattus norv
19	1804.5	27.5	2043	2	Q27IT6_DROSI	Q27it6 drosophila
20	1804.5	27.5	2043	2	Q27IT5_DROSI	Q27it5 drosophila
21	1803.5	27.4	2043	2	Q27IT9_DROSI	Q27it9 drosophila
22	1802.5	27.4	2043	2	Q27IT8_DROSI	Q27it8 drosophila
23	1802.5	27.4	2043	2	Q27IU2_DROME	Q27iu2 drosophila
24	1801.5	27.4	2043	2	Q27IU4_DROME	Q27iu4 drosophila
25	1800.5	27.4	2043	2	Q27IT4_DROSI	Q27it4 drosophila
26	1800.5	27.4	2043	2	Q27IT7_DROSI	Q27it7 drosophila
27	1800.5	27.4	2043	2	Q27IU3_DROME	Q27iu3 drosophila
28	1799.5	27.4	2043	2	Q27IU7_DROME	Q27iu7 drosophila
29	1798.5	27.4	2043	2	Q27IU1_DROSI	Q27iu1 drosophila
30	1798.5	27.4	2043	2	Q27IU0_DROSI	Q27iu0 drosophila
31	1794.5	27.3	2043	2	Q27IU6_DROME	Q27iu6 drosophila
32	1793.5	27.3	2043	2	Q27IU5_DROME	Q27iu5 drosophila
33	1793.5	27.3	2043	2	Q27IU9_DROME	Q27iu9 drosophila
34	1793.5	27.3	2043	2	Q27IU8_DROME	Q27iu8 drosophila
35	1788.5	27.2	1845	1	DCR1_CAEEL	P34529 caenorhabdi
36	1752	26.7	361	2	Q8R419_MOUSE	Q8r419 mus musculu
37	1710.5	26.0	1863	2	Q60MW6_CAEBR	Q60mw6 caenorhabdi
38	1090.5	16.6	1658	2	Q174T8_AEDAE	Q174t8 aedes aegyp
39	1076.5	16.4	1658	2	Q49LL4_AEDAE	Q49ll4 aedes aegyp
40	974.5	14.8	1715	2	Q291A3_DROPS	Q291a3 drosophila
41	953	14.5	197	2	Q5GIT5_ONCMY	Q5git5 oncorhynchu
42	951.5	14.5	1657	2	Q7Q073_ANOGA	Q7q073 anopheles g
43	947.5	14.4	1719	2	Q2Q3U0_DROYA	Q2q3u0 drosophila
44	947.5	14.4	1719	2	Q2Q3U4_DROYA	Q2q3u4 drosophila
45	944.5	14.4	1719	2	Q2Q3U2_DROYA	Q2q3u2 drosophila

ALIGNMENTS

RESULT 1

DICER_HUMAN

ID DICER_HUMAN Reviewed; 1912 AA.
AC Q9UPY3; O95943; Q9UQ02;
DT 25-OCT-2002, integrated into UniProtKB/Swiss-Prot.
DT 25-OCT-2002, sequence version 2.
DT 24-JUL-2007, entry version 61.
DE Endoribonuclease Dicer (EC 3.1.26.-) (Helicase with RNase motif)
DE (Helicase-MOI).
GN Name=DICER1; Synonyms=DICER, HERNA, KIAA0928;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=20246304; PubMed=10786632; DOI=10.1016/S0167-4781(99)00221-3;
RA Matsuda S., Ichigotani Y., Okuda T., Irimura T., Nakatsugawa S.,
RA Hamaguchi M.;
RT "Molecular cloning and characterization of a novel human gene (HERNA)
RT which encodes a putative RNA-helicase.";

RL Biochim. Biophys. Acta 1490:163-169(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Lung;
 RA Provost P., Dishart D., Doucet D., Hermansson A., Friendewey D.,
 RA Samuelsson B., Radmark O.;
 RT "RNA binding and processing by recombinant human Dicer.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=99246063; PubMed=10231032; DOI=10.1093/dnares/6.1.63;
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:63-70(1999).
 RN [4]
 RP SEQUENCE REVISION.
 RX MEDLINE=22158633; PubMed=12168954; DOI=10.1093/dnares/9.3.99;
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual
 RT curation of 330 KIAA cDNA clones.";
 RL DNA Res. 9:99-106(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 1238-1912.
 RC TISSUE=Lung;
 RX MEDLINE=99162526; PubMed=10051563; DOI=10.1073/pnas.96.5.1881;
 RA Provost P., Samuelsson B., Radmark O.;
 RT "Interaction of 5-lipoxygenase with cellular proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1881-1885(1999).
 RN [6]
 RP INTERACTION WITH PIWIL1.
 RX PubMed=14749716; DOI=10.1038/sj.embor.7400070;
 RA Tahbaz N., Kolb F.A., Zhang H., Jaronczyk K., Filipowicz W.,
 RA Hobman T.C.;
 RT "Characterization of the interactions between mammalian PAZ PIWI
 RT domain proteins and Dicer.";
 RL EMBO Rep. 5:189-194(2004).
 RN [7]
 RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT TYR-654, AND MASS
 RP SPECTROMETRY.
 RX PubMed=15592455; DOI=10.1038/nbt1046;
 RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
 RA Zha X.-M., Polakiewicz R.D., Comb M.J.;
 RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer
 RT cells.";
 RL Nat. Biotechnol. 23:94-101(2005).
 CC -!- FUNCTION: Involved in cleaving double-stranded RNA in the RNA
 CC interference (RNAi) pathway. It produces 21 to 23 bp dsRNAs
 CC (siRNAs) which target the selective destruction of homologous
 CC RNAs.
 CC -!- SUBUNIT: Interacts with PIWIL1.
 CC -!- INTERACTION:
 CC Q9UL18:EIF2C1; NbExp=2; IntAct=EBI-395506, EBI-527363;
 CC Q9UKV8:EIF2C2; NbExp=1; IntAct=EBI-395506, EBI-528269;

CC Q8CJG0:Elf2c2 (xeno); NbExp=2; IntAct=EBI-395506, EBI-528299;
 CC Q8TBY5:PIWIL1; NbExp=1; IntAct=EBI-395506, EBI-527417;
 CC Q15633:TARBP2; NbExp=4; IntAct=EBI-395506, EBI-978581;
 CC -!- SIMILARITY: Belongs to the helicase family.
 CC -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
 CC -!- SIMILARITY: Contains 1 helicase ATP-binding domain.
 CC -!- SIMILARITY: Contains 1 helicase C-terminal domain.
 CC -!- SIMILARITY: Contains 1 PAZ domain.
 CC -!- SIMILARITY: Contains 2 RNase III domains.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AB028449; BAA78691.1; ALT_INIT; mRNA.
 DR EMBL; AJ132261; CAB38857.2; -; mRNA.
 DR EMBL; AB023145; BAA76772.2; ALT_INIT; mRNA.
 DR UniGene; Hs.87889; -.
 DR HSSP; O67082; 1JFZ.
 DR IntAct; Q9UPY3; -.
 DR Ensembl; ENSG00000100697; Homo sapiens.
 DR KEGG; hsa:23405; -.
 DR HGNC; HGNC:17098; DICER1.
 DR HPA; HPA000694; -.
 DR MIM; 606241; gene.
 DR PharmGKB; PA38437; -.
 DR ArrayExpress; Q9UPY3; -.
 DR GermOnline; ENSG00000100697; Homo sapiens.
 DR GO; GO:0005622; C:intracellular; NAS:UniProtKB.
 DR GO; GO:0003725; F:double-stranded RNA binding; IDA:UniProtKB.
 DR GO; GO:0005515; F:protein binding; IPI:IntAct.
 DR GO; GO:0004525; F:ribonuclease III activity; IDA:UniProtKB.
 DR GO; GO:0030423; P:RNA interference, targeting of mRNA for des. . .;
 IEP:UniProtKB.
 DR InterPro; IPR014001; DEAD-like_N.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR001159; Ds_RNA_bd.
 DR InterPro; IPR005034; DUF283.
 DR InterPro; IPR014021; Helic_SF1/SF2_ATP_bd.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR003100; PAZ.
 DR InterPro; IPR000999; RNase_III.
 DR Gene3D; G3DSA:1.10.1520.10; RNase_III; 2.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00035; dsrm; 1.
 DR Pfam; PF03368; DUF283; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF02170; PAZ; 1.
 DR Pfam; PF00636; Ribonuclease_3; 2.
 DR SMART; SM00487; DEXDc; 1.
 DR SMART; SM00358; DSRM; 1.
 DR SMART; SM00490; HELICc; 1.
 DR SMART; SM00535; RIBOc; 2.
 DR PROSITE; PS50137; DS_RBD; 1.
 DR PROSITE; PS51192; HELICASE_ATP_BIND_1; 1.
 DR PROSITE; PS51194; HELICASE_CTER; 1.
 DR PROSITE; PS50821; PAZ; 1.
 DR PROSITE; PS00517; RNASE_3_1; 1.

DR PROSITE; PS50142; RNASE_3_2; 2.
PE 1: Evidence at protein level;
KW ATP-binding; Endonuclease; Helicase; Hydrolase; Nuclease;
KW Nucleotide-binding; Phosphorylation; Repeat; RNA-binding;
KW RNA-mediated gene silencing.
FT CHAIN 1 1912 Endoribonuclease Dicer.
FT /FTId=PRO_0000180470.
FT DOMAIN 41 217 Helicase ATP-binding.
FT DOMAIN 423 592 Helicase C-terminal.
FT DOMAIN 881 1032 PAZ.
FT DOMAIN 1266 1393 RNase III 1.
FT DOMAIN 1656 1814 RNase III 2.
FT DOMAIN 1839 1904 DRBM.
FT NP_BIND 34 41 ATP (Potential).
FT MOTIF 165 168 DECH box.
FT MOD_RES 654 654 Phosphotyrosine.
FT CONFLICT 65 80 VLLTKELSYQIRGDFS -> STTLLKSCLYLDLGETSA
FT (in Ref. 1).
FT CONFLICT 179 179 I -> F (in Ref. 1).
FT CONFLICT 185 185 N -> I (in Ref. 1).
FT CONFLICT 204 204 C -> W (in Ref. 1).
FT CONFLICT 208 208 E -> D (in Ref. 1).
FT CONFLICT 213 213 I -> F (in Ref. 1).
FT CONFLICT 383 384 QQ -> HS (in Ref. 1).
FT CONFLICT 482 483 KQ -> NT (in Ref. 1).
FT CONFLICT 599 599 D -> H (in Ref. 1).
SQ SEQUENCE 1912 AA; 217628 MW; 996399DB4B074F21 CRC64;

Query Match 100.0%; Score 6572; DB 1; Length 1912;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIVGPPMSCVRLAERVVALICCEKLHKIGELDDHLMVPVGKETVKYEEELDLHDEEETSV 60
|
Db 667 ASIVGPPMSCVRLAERVVALICCEKLHKIGELDDHLMVPVGKETVKYEEELDLHDEEETSV 726
Qy 61 PGRPGSTKRRQCYPKAIPCELRDSYPRPDQPCYLYVIGMVLTTPLPDELNFRRRKLYPPE 120
|
Db 727 PGRPGSTKRRQCYPKAIPCELRDSYPRPDQPCYLYVIGMVLTTPLPDELNFRRRKLYPPE 786
Qy 121 DTTRCFGILTAKPIPHFPVYTRSGEVTISIELKKSGFMLSQMLELITRLHQYIFSH 180
|
Db 787 DTTRCFGILTAKPIPHFPVYTRSGEVTISIELKKSGFMLSQMLELITRLHQYIFSH 846
Qy 181 ILRLEKPALEFKPTDADSAYCVLPLNVVNDSSSTLDIDFKFMEDIEKSEARIGIPSTKYTK 240
|
Db 847 ILRLEKPALEFKPTDADSAYCVLPLNVVNDSSSTLDIDFKFMEDIEKSEARIGIPSTKYTK 906
Qy 241 ETPFVFKLEDYQDAVIIPRYRNFDQPHRFYVADVYTDLTPLSKFPSPEYETFAEYYKTKY 300
|
Db 907 ETPFVFKLEDYQDAVIIPRYRNFDQPHRFYVADVYTDLTPLSKFPSPEYETFAEYYKTKY 966
Qy 301 NDLTLNLNQPLLDVDHTSSRLNLLTPRHLNQKGKALPLSSAEKRKAKWESLQNKQILVPE 360
|
Db 967 NDLTLNLNQPLLDVDHTSSRLNLLTPRHLNQKGKALPLSSAEKRKAKWESLQNKQILVPE 1026
Qy 361 LCAIHPIPASLWRKAVCLPSILYRLHCLLTAEELRAQTASDAGVGVRSPLADFRYPNLDF 420

Db	1027	 LCAIHPIPASLWRKAVCLPSILYRLHCLLTAEELRAQTASDAGVGVRSLPADFRYPNLDF	1086
Qy	421	GWKKSIDSKSFISISNSSSAENDNYCKHSTIVPENAAHQGANRTSSLENHDQMSVNCRTL	480
Db	1087	GWKKSIDSKSFISISNSSSAENDNYCKHSTIVPENAAHQGANRTSSLENHDQMSVNCRTL	1146
Qy	481	LSESPGKLHVEVSADLTAINGLSYNQNLANGSYDLANRDFCQGNQLNYYKQEIPVQPTTS	540
Db	1147	LSESPGKLHVEVSADLTAINGLSYNQNLANGSYDLANRDFCQGNQLNYYKQEIPVQPTTS	1206
Qy	541	YSIQNLYSYENQPQPSDECTLLSNKYLDGNANKSTSDGSPVMAVMPGTTDTIQVLKGRMD	600
Db	1207	YSIQNLYSYENQPQPSDECTLLSNKYLDGNANKSTSDGSPVMAVMPGTTDTIQVLKGRMD	1266
Qy	601	SEQSPSIGYSSRTLGNPGLILQALTLSNASDGFNLERLEMLGDSFLKHAITTYLFCTYP	660
Db	1267	SEQSPSIGYSSRTLGNPGLILQALTLSNASDGFNLERLEMLGDSFLKHAITTYLFCTYP	1326
Qy	661	DAHEGRLSYMRSKKVSNCNLYRLGKKKGLPSRMVVSIFDPPVNWLP PGYVVNQDKSNTDK	720
Db	1327	DAHEGRLSYMRSKKVSNCNLYRLGKKKGLPSRMVVSIFDPPVNWLP PGYVVNQDKSNTDK	1386
Qy	721	WEKDEMTKDCMLANGKLDEDEYEEDEEEESLMWRAPKEEADYEDDFLEYDQEHIRFIDNM	780
Db	1387	WEKDEMTKDCMLANGKLDEDEYEEDEEEESLMWRAPKEEADYEDDFLEYDQEHIRFIDNM	1446
Qy	781	LMGSGAFVKKISLSPFSTTDSAYEWKMPKKSSLGSMFSSDFEDFDYSSWDAMCYLDPSK	840
Db	1447	LMGSGAFVKKISLSPFSTTDSAYEWKMPKKSSLGSMFSSDFEDFDYSSWDAMCYLDPSK	1506
Qy	841	AVEEDDFVVGFWNPSEENCVDGTGKQSI SYDLHTEQCIADKSIADCVEALLGCYLTSCE	900
Db	1507	AVEEDDFVVGFWNPSEENCVDGTGKQSI SYDLHTEQCIADKSIADCVEALLGCYLTSCE	1566
Qy	901	RAAQFLCFLGLKVLVPIKRTDREKALCPTRENFNSQQKNLSVSCAAASVASSRSSLVKD	960
Db	1567	RAAQFLCFLGLKVLVPIKRTDREKALCPTRENFNSQQKNLSVSCAAASVASSRSSLVKD	1626
Qy	961	SEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKIN YRFKNKAYLLQAFTHASYHYNT	1020
Db	1627	SEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKIN YRFKNKAYLLQAFTHASYHYNT	1686
Qy	1021	ITDCYQRLEFLGDAILDYLITKHLYEDPRQHSPGVLTDLRSALVNNTIFASLAVKYDYHK	1080
Db	1687	ITDCYQRLEFLGDAILDYLITKHLYEDPRQHSPGVLTDLRSALVNNTIFASLAVKYDYHK	1746
Qy	1081	YFKAVSPELFHVIDDFVQFQLEKNEMQGMSELRRSEED EEEKEEDIEVPKAMGDIFESLA	1140
Db	1747	YFKAVSPELFHVIDDFVQFQLEKNEMQGMSELRRSEED EEEKEEDIEVPKAMGDIFESLA	1806
Qy	1141	GAIYMDSGMSLETVWQVYYPMMRPLIEKFSANVPRSPVRELLEMEPETAKFSPAERTYDG	1200
Db	1807	GAIYMDSGMSLETVWQVYYPMMRPLIEKFSANVPRSPVRELLEMEPETAKFSPAERTYDG	1866
Qy	1201	KVRVTVEVVGKGKFKGVGRSYRIAKSAAARRALRSLKANQPQVPNS	1246

Db 1867 KVRVTVEVVGKGKFKGVGRSYRIAKSAAARRALRSLKANQPQVPNS 1912

RESULT 2

Q6TUI4_BOVIN

ID Q6TUI4_BOVIN Unreviewed; 1923 AA.
AC Q6TUI4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 24-JUL-2007, entry version 35.
DE Dicer.
GN Name=dicer;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Golding M.C., Long C.R., Westhusin M.E.;
RT "Overexpression of Bovine Dicer in Mammalian Cells.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC -----
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CC -----
DR EMBL; AY386968; AAR26432.1; -; mRNA.
DR UniGene; Bt.45343; -.
DR Ensembl; ENSBTAG00000012852; Bos taurus.
DR KEGG; bta:337871; -.
DR GO; GO:0005622; C:intracellular; IEA:InterPro.
DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA:InterPro.
DR GO; GO:0004386; F:helicase activity; IEA:InterPro.
DR GO; GO:0004525; F:ribonuclease III activity; IEA:InterPro.
DR GO; GO:0006396; P:RNA processing; IEA:InterPro.
DR InterPro; IPR014001; DEAD-like_N.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001159; Ds_RNA_bd.
DR InterPro; IPR005034; DUF283.
DR InterPro; IPR014021; Helic_SF1/SF2_ATP_bd.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR000999; RNase_III.
DR Gene3D; G3DSA:1.10.1520.10; RNase_III; 2.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF03368; DUF283; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF02170; PAZ; 1.
DR Pfam; PF00636; Ribonuclease_3; 2.
DR SMART; SM00487; DEXDc; 1.
DR SMART; SM00358; DSRM; 1.
DR SMART; SM00490; HELICc; 1.
DR SMART; SM00535; RIBOc; 2.
DR PROSITE; PS50137; DS_RBD; 1.
DR PROSITE; PS51192; HELICASE_ATP_BIND_1; 1.